AMENDMENTS TO THE SPECIFICATION

Please replace the title with the following:

METHODS FOR ~~USING CO-REGULATED GENESETS TO ENHANCE DETECTION AND CLASSIFICATION OF GENE EXPRESSION PATTERNS~~ REMOVING ARTIFACT FROM BIOLOGICAL PROFILES

Please replace the paragraph starting on page 7, line 22, with the following:

[[Fig. 4B]] Figs. 4B-4D ~~illustrates~~ illustrate three main clusters of yeast genes with distinct temporal behavior. The first group (early) shown in Fig. 4B is responding to the STE12 transcription factor, the second group (adaptive) shown in Fig. 4C contains members of the main signaling pathway such as STE2, and the third group (cell cycle) shown in Fig. 4D is associated with the cell cycle perturbations inflicted by the mating response.

Please replace the paragraph starting on page 7, line 32, with the following:

~~Fig~~ Figs. 8A-E ~~shows~~ show amplitudes of the individual elements of the projected profile for a comparison with FK506 at 16μg/ml with: FIG. 8A, HU at 3.1 mM; FIG. 8B, FK506 at 50 μg/ml; FIG. 8C, FK506 at 1 μg/ml; FIG. 8D, deletion of the GCN4 gene and FK506 at 50 μg/ml; and FIG. 8E, deletion of cna and FK506 at 50 μg/ml (FIG. 8E).

Please replace the paragraph starting on page 31, line 18, with the following:

~~Figure 4B gives~~ Figures 4B-4D give an example of clustering of genes by their temporal response profiles across several time points. The experiment here was activation of the yeast mating pathway (same strains, methods, etc. as described earlier) with the yeast α mating pheromone. Expression responses for all yeast genes ratioed to control (mock treatment) baseline were measured immediately after treatment, and at 15 minutes after treatment, 30, 45, 60, 90, and 120 minutes after treatment. This time series of experiments provided the experiment set for clustering analysis. Each line represents one experiment. A

line with an asterisk represents an experiment that was given low weight in clustering operation. Three of the main cluster groups are illustrated in ~~FIG. 4B~~ FIGS. 4B-4D, showing systematically distinct temporal behavior. The first group (early, Fig. 4B) is responding to the STE12 transcription factor, the second group (adaptive, Fig. 4C) contains members of the main signaling pathway such as STE2 and STE12 itself that fatigue (show decreasing response) with continued treatment, and the third group (cell cycle, Fig. 4D) is associated with the cell cycle perturbations inflicted by the mating response.

Please replace the paragraph starting on page 31, line 32, with the following:

It is possible to define augmented basis vectors whose indices cover constituents *and* time points. Projection onto these basis vectors picks out the amplitudes of response in specific gene groups *and* of specific temporal profiles. Thus, for example, we could efficiently detect responses such as those shown in the third group in ~~FIG. 4B~~ FIG. 4D by projecting a time series of expression profiles onto an augmented basis vector whose elements were nonzero only for the genes included in the third group, and whose nonzero amplitudes varied over the time index according to the average of the temporal response in the third group.